

Listing of Claims:

1-138 (canceled)

139. (previously presented) A method of identifying a set of oligonucleotides for use in an *in vitro* recombination procedure, the method comprising:

(a) providing data identifying sequences of two or more parental polypeptides or parental nucleic acids that encode the polypeptides;

(b) computationally selecting one or more cross-over sites on the sequences based on structural information about the parental polypeptides or polypeptides encoded by the parental nucleic acids; thereby defining one or more recombinant polypeptides or recombinant nucleic acids that result from cross-overs between the parental polypeptides or nucleic acids at the one or more cross-over sites;

(c) selecting at least one of the recombinant polypeptides or recombinant nucleic acids by computationally assessing structural stability of at least some of the recombinant polypeptides or polypeptides encoded by the recombinant nucleic acids; and

(d) computationally identifying one or more oligonucleotides for *in vitro* recombination by choosing at least one portion of at least one of the recombinant polypeptides or recombinant nucleic acids selected in (c) which at least one portion corresponds to the one or more oligonucleotides identified for *in vitro* recombination.

140. (previously presented) The method of claim 139, wherein the structural information employed in (b) comprises information depicting the three-dimensional structure of at least a portion of the parental polypeptides or polypeptides encoded by the parental nucleic acids.

141. (previously presented) The method of claim 139, wherein (b) comprises selecting cross-over points that correspond to overlapping amino acids in the parental polypeptides.

142. (previously presented) The method of claim 139, wherein (b) comprises selecting cross-over points at sites that will preserve selected subunits, domains, or motifs in the parental polypeptides.

143. (previously presented) The method of claim 139, wherein (b) comprises selecting cross-over points at sites chosen to maintain or disrupt one or more structural relationships between two or more amino acids in the parental polypeptides.

144. (previously presented) The method of claim 139, further comprising performing an additional genetic operation on one or more of the parental or recombinant polypeptides or the parental or recombinant nucleic acids.

145. (previously presented) The method of claim 144, wherein the genetic operation is selected from the group consisting of multiplication, mutation, fragmentation, and ligation.

146. (previously presented) The method of claim 139, wherein the two or more parental polypeptides or parental nucleic acids comprise naturally occurring polypeptides or naturally occurring nucleic acids that encodes polypeptides.

147. (previously presented) The method of claim 139, wherein (c) comprises computationally assessing three-dimensional structural stability of at least some of the recombinant polypeptides or polypeptides encoded by the recombinant nucleic acids.

148. (previously presented) A computer program product comprising a machine readable medium on which is provided program instructions for identifying a set of oligonucleotides for use in an *in vitro* recombination procedure, the program instructions comprising:

(a) code for providing data identifying sequences of two or more parental polypeptides or parental nucleic acids that encode the polypeptides;

(b) code for selecting one or more cross-over sites on the sequences based on structural information about the parental polypeptides or polypeptides encoded by the parental nucleic acids; thereby defining one or more recombinant polypeptides or recombinant nucleic acids that result from cross-overs between the parental polypeptides or nucleic acids at the one or more cross-over sites;

(c) code for selecting at least one of the recombinant polypeptides or recombinant nucleic acids by assessing structural stability of at least some of the recombinant polypeptides or polypeptides encoded by the recombinant nucleic acids; and

(d) code for identifying one or more oligonucleotides for *in vitro* recombination by choosing at least one portion of at least one of the recombinant polypeptides or recombinant nucleic acids selected in (c) which at least one portion corresponds to the one or more oligonucleotides identified for *in vitro* recombination.

149. (previously presented) The computer program product of claim 148, wherein the structural information employed in (b) comprises information depicting the three-dimensional

structure of at least a portion of the parental polypeptides or polypeptides encoded by the parental nucleic acids.

150. (previously presented) The computer program product of claim 148, wherein (b) comprises code for selecting cross-over points that correspond to overlapping amino acids in the parental polypeptides.

151. (previously presented) The computer program product of claim 148, wherein (b) comprises code for selecting cross-over points at sites that will preserve selected subunits, domains, or motifs in the parental polypeptides.

152. (previously presented) The computer program product of claim 148, wherein (b) comprises code for selecting cross-over points at sites chosen to maintain or disrupt one or more structural relationships between two or more amino acids in the parental polypeptides.

153. (previously presented) The computer program of claim 148, further comprising code for performing an additional genetic operation on one or more of the parental or recombinant polypeptides or the parental or recombinant nucleic acids.

154. (previously presented) The computer program product of claim 153, wherein the genetic operation is selected from the group consisting of multiplication, mutation, fragmentation, and ligation.

155. (previously presented) The computer program product of claim 148, wherein at least one of the parental polypeptides or the parental nucleic acids comprise a naturally occurring polypeptide or a naturally occurring nucleic acid that encodes a polypeptide.

156. (previously presented) The computer program product of claim 148, wherein (c) comprises code for assessing three-dimensional structural stability of at least some of the recombinant polypeptides or polypeptides encoded by the recombinant nucleic acids.

157. (previously presented) The method of claim 139, wherein the oligonucleotides identified in (d) are “bridging” oligonucleotides.

158. (previously presented) The method of claim 139, further comprising aligning the two or more parental polypeptides or parental nucleic acids prior to computationally selecting one or more cross-over sites on the sequences.

159. (previously presented) The method of claim 139, wherein the recombinant polypeptides or recombinant nucleic acids that result from the cross-overs comprise contiguous sequences of multiple amino acids or nucleotides from the two or more of the parental polypeptides or parental nucleic acids.

160. (new) The computer program product of claim 148, wherein the code for identifying one or more oligonucleotides in (d) identifies “bridging” oligonucleotides.

161. (new) The computer program product of claim 148, further comprising code for aligning the two or more parental polypeptides or parental nucleic acids prior to computationally selecting one or more cross-over sites on the sequences.

162. (new) The computer program product of claim 148, wherein the recombinant polypeptides or recombinant nucleic acids that result from the cross-overs comprise contiguous sequences of multiple amino acids or nucleotides from the two or more of the parental polypeptides or parental nucleic acids.